AD_____

GRANT NUMBER DAMD17-94-J-4290

TITLE: Genetic Abnormalities in Breast Cancer Tumors and Relationships to Environmental and Genetic Risk Factors Using Twins

PRINCIPAL INVESTIGATOR: Thomas M. Mack, M.D.

CONTRACTING ORGANIZATION: University of California
Los Angeles, California   90033

REPORT DATE: September 1998

TYPE OF REPORT: Annual

PREPARED FOR: Commander
U.S. Army Medical Research and Materiel Command
Fort Detrick, Frederick, Maryland   21702-5012

DISTRIBUTION STATEMENT: Approved for public release;
distribution unlimited

The views, opinions and/or findings contained in this report are those of the author(s) and should not be construed as an official Department of the Army position, policy or decision unless so designated by other documentation.

19990813 049

REPORT DOCUMENTATION PAGE

Public reporting burden for this collection of information is estimated to average 1 hour per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden, to Washington Headquarters Services, Directorate for Information Operations and Reports, 1215 Jefferson Davis Highway, Suite 1204, Arlington, VA 22202-4302, and to the Office of Management and Budget, Paperwork Reduction Project (0704-0188), Washington, DC 20503.

1. AGENCY USE ONLY *(Leave blank)*	2. REPORT DATE September 1998	3. REPORT TYPE AND DATES COVERED Annual (1 Oct 97 – 30 Sep 98)

4. TITLE AND SUBTITLE
Genetic Abnormalities in Breast Cancer Tumors and Relationships to Environmental and Genetic Risk Factors Using Twins

5. FUNDING NUMBERS
DAMD17-94-J-4290

6. AUTHOR(S)

Thomas M. Mack, M.D.

7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES)

University of Southern California
Los Angeles, California 90033

8. PERFORMING ORGANIZATION REPORT NUMBER

9. SPONSORING/MONITORING AGENCY NAME(S) AND ADDRESS(ES)
Commander
U.S. Army Medical Research and Materiel Command
Fort Detrick, Frederick, Maryland 21702-5012

10. SPONSORING/MONITORING AGENCY REPORT NUMBER

11. SUPPLEMENTARY NOTES

12a. DISTRIBUTION / AVAILABILITY STATEMENT

Approved for public release; distribution unlimited

12b. DISTRIBUTION CODE

13. ABSTRACT *(Maximum 200*

Activities included 1) acquisition of archived tissue blocks on breast cancer concordant twin pairs (206 MZ and 130 DZ) and discordant pairs (548 MZ); 2) immunohistochemistry to detect the level of expression of biomarkers (p53, HER-2/*neu*, ER, and PR) in the tumor tissue; 3) DNA sequencing of the p53 gene; 4) FISH to detect amplification of HER-2/*neu*; and 5) analysis of the association of environmental and genetic factors with the development of these markers. Blocks from 330 twins (206 in concordant pairs and 124 in discordant pairs) have been received. Based on 41 concordant pairs, intra-pair analyses showed that ER was the biomarker most likely to be identical within the pair (Kappa=0.42) and HER-2/*neu* was the least likely (Kappa=0.03). The low agreement suggests that environmental factors are likely to play a role in the development of some of these tumor markers. DNA sequencing of the p53 gene has been completed for 50 cases, with 25 having at least one mutation. FISH has been completed on 100 cases. During the next year (for which we have a no cost extension), collection of tissue blocks, immunohistochemistry, sequencing of the p53 gene and FISH to determine HER-2/*neu* gene amplification will be completed. Additional epidemiologic analyses will be completed to further investigate the relationship of risk factors to tumor marker development.

14. SUBJECT TERMS
Breast Cancer Twins, genetics, p53, HER-2/neu, ER, PR, immunohistochemistry, DNA sequencing, epidemiology, FISH

15. NUMBER OF PAGES
17

16. PRICE CODE

17. SECURITY CLASSIFICATION OF REPORT	18. SECURITY CLASSIFICATION OF THIS PAGE	19. SECURITY CLASSIFICATION OF ABSTRACT	20. LIMITATION OF ABSTRACT
Unclassified	Unclassified	Unclassified	Unlimited

NSN 7540-01-280-5500

Standard Form 298 (Rev. 2-89)
Prescribed by ANSI Std. Z39-18
298-102

FOREWORD

Opinions, interpretations, conclusions and recommendations are those of the author and are not necessarily endorsed by the U.S. Army.

_____ Where copyrighted material is quoted, permission has been obtained to use such material.

_____ Where material from documents designated for limited distribution is quoted, permission has been obtained to use the material.

_____ Citations of commercial organizations and trade names in this report do not constitute an official Department of Army endorsement or approval of the products or services of these organizations.

_____ In conducting research using animals, the investigator(s) adhered to the "Guide for the Care and Use of Laboratory Animals," prepared by the Committee on Care and Use of Laboratory Animals of the Institute of Laboratory Resources, National Research Council (NIH Publication No. 86-23, Revised 1985).

__/__ For the protection of human subjects, the investigator(s) adhered to policies of applicable Federal Law 45 CFR 46.

_____ In conducting research utilizing recombinant DNA technology, the investigator(s) adhered to current guidelines promulgated by the National Institutes of Health.

_____ In the conduct of research utilizing recombinant DNA, the investigator(s) adhered to the NIH Guidelines for Research Involving Recombinant DNA Molecules.

_____ In the conduct of research involving hazardous organisms, the investigator(s) adhered to the CDC-NIH Guide for Biosafety in Microbiological and Biomedical Laboratories.
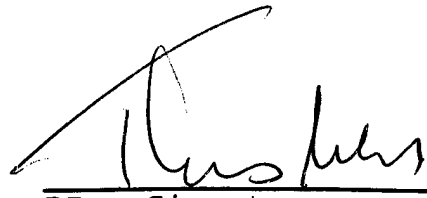
PI - Signature   Date

Table of Contents

Page

ANNUAL REPORT

        1. Data management
        2. Acquisition of Archived Blocks
        3. Laboratory Procedures
        4. Epidemiologic Analyses
        5. Results to date

A. INTRODUCTION

Abnormalities relating to the p53 gene are one of the most commonly found genetic aberration in breast cancer tumors, and include overexpression of p53 protein, loss of heterozygosity at the p53 locus, and specific mutations in the p53 gene. However, it is unknown why some tumors have these changes and others do not. Further, little is known about what factors are involved in the interaction of oncogenes such as HER-2/neu with p53.

While investigators in previous studies have attempted to link p53 abnormalities to tumor histology, survival time, estrogen and progesterone receptor status, Her-2/neu, and, in some cases, risk factors for breast cancer, none has studied all of these factors within a large population of twins. These subjects offer great potential for distinguishing the role of predisposing genetic factors from environmental exposures. Specifically we will address the following issues in this study: 1) Are genetically similar tumors more likely to occur among identical twins than among fraternal twins? 2) Do environmental factors predispose to concordance or discordance of genetic abnormalities? 3) Do fraternal twins, concordant for environmental exposures, tend to be discordant for genetic abnormalities, suggesting that other predisposing genetic factors that can be identified? 4) Among identical twins discordant for disease, are specific environmental factors more related to tumors with a genetic abnormality than those without?

Three methods have been commonly used to detect p53 abnormalities: immunohistochemical methods of detecting overexpression of the mutant p53 protein, polymerase chain reaction (PCR) techniques for the detection and sequencing of specific p53 mutations, and Southern blots to detect loss of heterozygosity (LOH) at the p53 gene locus. Studies have indicated that 50-60% of breast tumors may have LOH in the 17p region; there may be overexpression of the p53 mutant protein in 27-54% of all breast tumors (3). Specific mutations in the p53 gene usually occur in the highly conserved exons 5-8 (4,5). Twenty-five percent have been shown to occur in codons 245, 248, 273, and 282 (6). From collaborative efforts of specific p53 mutations in more that 30 types of cancer it has been shown that different types of cancer evince different patterns of DNA base substitutions (7).

Rarely have all types of abnormalities been investigated within the same tumor tissue, but a few studies provide information on the correlations between them. Overexpression of the mutant p53 protein product has been seen in association with mutation of the p53 gene (8) but not invariably (9). LOH and overexpression of the p53 protein have been found to occur independently (9,10,11). The mechanism by which dysfunction in the p53 gene leads to malignant transformation is therefore unclear.

Under one hypothesis it would be necessary for both copies of the p53 gene to be inactivated by loss or mutation to prevent the transcription of the normal or 'wild-type' protein and hence prevent normal function of the gene. The failure by some investigators to demonstrate damage to or loss of both copies of the p53 gene suggests that additional steps or other mechanisms must precede malignant transformation. For example, under a hypothesis of co-dominance, a stable

mutant protein might bind to and inactivate any wild-type protein produced (12). Strong immunohistochemical staining for p53 in normal cells has been found in a mother and daughter with a family history of breast cancer (13). However, no p53 overexpression was found in fibroblasts from individuals from families with the Li-Fraumeni syndrome who had germline DNA mutations of the p53 gene (14). Thus another event (apart from damage to p53) sometimes may be necessary for expression of mutant protein, or only certain mutations in p53 may be related to overexpression of the mutant protein and subsequent malignant transformation.

Another mechanism by which the normal function of p53 gene may be interrupted is by nuclear exclusion (15). When p53 protein is found in the nucleus of cells, mutations in the gene are usually found, whereas when the protein is found in the cytoplasm, mutations are generally not found. If the protein is sequestered in the cytoplasm (by binding with heat shock proteins) then it may be unable to regulate nuclear division. Some studies have shown p53 protein to occur in the cytoplasm of lobular breast cancers (16).

When p53 mutations in germline tissue were found in members of Li-Fraumeni families (17), efforts to detect germline mutations in other high-risk families were intensified, largely without success (18, 19, 20). While these studies were based on small numbers of families: 5 (18) and 25 (19), or cases: 19 individuals with bilateral disease (20). This failure has led to the presumption that environmental factors or other genes may also determine the abnormalities in the p53 gene that lead to breast cancer (21). In any event, the inactivation or disabling of the p53 gene appears to be an important step in a large proportion of breast cancer cases, and studies have shown it to be an early step, present in *situ* tumors and maintained throughout all stages of tumor progression (8).

Since the etiology of breast cancer appears to be complex and heterogenous, other genes, especially oncogenes, may sometimes interact with p53 in the development and progression of breast cancer. HER-2/neu (or also referred to as c-erbB-2), located on the long arm of chromosome 17 (17q12-21.32) has been shown to occur in 20% of invasive breast cancer tumors and in 50% of all ductal carcinoma in situ (22). Studies that have examined the association of p53 with HER-2/neu have produced mixed results; at least four have found the two to be correlated (23, 24, 25, 26), while others have not (27, 28). Barbareschi et al. (26) suggest that p53 and HER-2/neu alterations may occur independently and at an early stage of tumor progression. Escape from hormonal control may be associated with HER-2/neu overexpression (which has been related to estrogen receptor negative tumors); while alterations in p53 may induce a high proliferation rate, leading to tumor progression and further opportunities for genetic damage.

The association of p53 abnormalities and HER-2/neu overexpression with estrogen and progesterone receptor status, histology, progression, and patient survival may provide insights into the mechanisms of tumor development and progression. While some studies have linked p53 overexpression to tumors with a more aggressive phenotype (28), it may be that LOH is more critical to tumor progression than any specific mutation (11). Nuclear p53 expression has been associated with tumors of aggressive (ductal) as well as less aggressive (medullary) histology (16); however neither LOH nor specific mutation sequences were assessed. HER-2/neu is

generally found in association with a poorer prognosis (29).

The relationship of p53 and HER-2/neu overexpression to environmental and other genetic risk factors has not been extensively studied. A higher proportion of tumors with p53 protein expression in familial than in sporadic cases has been reported (30). p53 has been associated with low levels of estrogen receptors (23, 26, 28) and late age at first full term pregnancy has been linked to the prevalence of estrogen receptors (McTiernan et al., 1986). An effect of breast-feeding on risk has been found to be dependent on expression of HER-2/neu (32).

To assess the interrelationships of tumor suppressor genes, oncogenes, specific mutations, loss of heterozygosity, and protein overexpression, it is essential that all factors be examined in the same material. This study presents the opportunity to study the several characteristics of breast cancer tumors in a large group of familial cases--concordant twin pairs--and relate these findings to genetic identity and to environmental risk factors. Secondly, a large number of disease discordant identical twin pairs offers the opportunity to further study association of environmental factors with specific genetic changes in breast cancer tumors.

B. BODY

Work done during the fourth year of the project has included the following:
1) Data management

2) Acquisition of Archived Tissue Blocks
    a) Ongoing contact with female twins (concordant MZ and DZ pairs, and discordant MZ pairs) from the International Twin Registry to obtain consent and release forms for acquisition of tissue blocks.
    b) Ongoing correspondence with hospitals to borrow tissue blocks and return them after slides have been made.

3) Laboratory procedures
    a) Processing: Logging in of received blocks and slides in database and processing of tissue blocks to cut and store slides.
    b) p53, HER-2/neu, and estrogen/progesterone receptor immunohistochemistry.
    c) DNA sequencing of the p53 gene from concordant pairs.
    d) FISH

4) Epidemiologic Analyses

5) Results

1). Data Management
A data management system using SAS was set up in the first year of the study and has been used to monitor the correspondence and follow-up efforts with the twins and their hospitals. The

laboratory information and the epidemiologic questionnaire information obtained from the twins when they first became part of the Registry have been linked using SAS datasets.

2). Acquisition of Archived Tumor Blocks
a. Contact with Twins
Three groups of twins have been contacted and results are shown in Table 1. There are a total of 1,220 cases for whom we are seeking archived tissue blocks. Our procedures for contacting the twins are the same for each group. Beginning with those who were diagnosed after 1975 and for whom we had already obtained pathology reports, we sent a letter explaining the study, the informed consent, and a release form to each twin for her signature. If we determined that a twin was deceased, these forms were sent to her next of kin. If we did not receive a response from a twin after 4 weeks, we have called the twin to be sure they received the forms and to answer any questions. Additional follow-up has been performed as required. For those with diagnosis dates before 1975, we called the hospitals first to determine if the tissue blocks were still available, before initiating the correspondence with the twin. Of the 85 hospitals called, blocks were available for approximately 30%.

b. Correspondence with Hospitals
Once the signed informed consent and release forms were obtained from a twin, a letter was sent to the hospital along with the release form requesting the tissue blocks, including one that was most representative of the tumor and one that contained normal tissue, such as a lymph node. If the hospital's policies prohibited sending the blocks, we requested that 20 unstained slides be cut from each of the blocks specified, and sent to us. For hospitals not responding follow-up efforts were initiated.

3). Laboratory Procedures

a. Processing: Once the blocks (or slides) are received, they are transferred to Dr. Press's Laboratory in padded envelopes which have the Twin ID number, name of submitting hospital, and number of blocks and/or slides provided. This information is logged into a master data file. Variables in this file include information the characteristics of the tissue, number of blocks, number of nodes sampled, and patient information. One H&E slide is cut from each block submitted. Since numerous blocks are sent with some specimens, this enables us to pick a block that is most representative of the tumor and one that is most representative of normal tissue. The 20 unstained slides are then cut from the chosen blocks and are then coated with paraffin so that antigenicity is not lost during storage. After this process has been completed, the blocks are sent back to the hospitals.

b. Immunohistochemistry: p53, HER-2/neu, ER and PR
When a specimen is selected to be stained, two slides per analysis are taken. One is for the antibody of interest and the other is used as a negative control. A positive control is used for every antibody on each day's run. The antibodies are scored on the basis of intensity of staining. HER-2/neu, being a membrane protein, is scored as low (+), over-expressed (++), or highly over-expressed (+++). A tumor was considered to be positive if the staining was either over-expressed

or highly overexpressed. P53, ER, and PR, which are nuclear proteins, are scored both by staining intensity and by percentage of cells with that particular intensity, i.e. (27%, +++), (33%, ++), (10%, +). For the initial analyses, we considered a tumor to be positive if more than 10% of the cells were positive.

c. DNA sequencing of the p53 gene: Our original plan was to do SSCP and then sequence only the portion of the gene with a mutation indicated by SSCP. However, in order to avoid the problems with lack of sensitivity inherent in the SSCP process, and since the technology for sequencing the gene has advanced since the grant was written we are now sequencing the entire gene directly, and eliminating the SSCP process. DNA yield is lower in the paraffinized tissue than in frozen tissue and the sequencing gives weaker peaks. This has required us to request more material for some cases.

d. Fluorescence In Situ Hybridization (FISH). FISH is a method using DNA probes to localize genes in cytogenetic chromosomal spreads, in cytologic preparations of whole cells, or in histologic sections of tissue. Hybridization of the probes to their complementary genetic elements in cells is recognized by visualizing a fluorescence signal in cell nuclei with a fluorescence microscope. Initially, in our preliminary studies we used a series of 10 established breast cancer cell lines to confirm that each cell line, known to be amplified by Southern hybridization data, was amplified by FISH. The probe for HER-2/*neu* hybridized with both metaphase and interphase DNA to yield signals that are proportional with the known gene amplification level of the cell lines.

4). Epidemiologic Analyses
The laboratory findings will be linked to environmental factors obtained from, a detailed questionnaire that was sent to all of the breast cancer twins and co-twins, which covers reproductive, developmental, and putative environmental breast cancer risk factors. Because the questionnaire included many questions about the co-twin, pairs in which only one twin responded can be used in the analysis. We will address the following objectives:
a) Within the concordant pairs in each zygosity group, determine if discordance in genetic abnormalities in tumor tissue is associated with discordance in environmental risk factors.
b) Within the MZ discordant pairs, determine if discordance in breast cancer is associated with discordance in environmental risk factors.
c) Within the MZ discordant pairs, determine if the relationship between environmental risk factors and breast cancer is the same for tumors with and without somatic abnormalities.

5). Results
a. Status of block accrual (Table 1)

We have resolved 723 (an increase of 153 from a year ago) cases at this time with tissue blocks obtained from 330 (an increase of 54 from a year ago). The largest group pending is with the effort to obtain the consent and release form from the patient or next of kin. We have been making extensive follow-up efforts on this group and for those who cannot be located, and for those who are known to be deceased with no next of kin identified, we will be sending a request

for the tissue blocks directly to the hospital. Currently we have 48 requests pending with hospitals and have another 56 completed consent forms which we will be sending to the identified hospitals. We are also in the process of returning blocks to the hospitals after we have completed our laboratory studies with them.

1) **MZ concordant twins:** 206 pairs of identical female twins, concordant for breast cancer, were initially selected to obtain archived tissue blocks. From these 412 cases we have obtained tissue blocks from 167 or 40.5%. We have continued to follow-up our contacts with these twins and their next-of-kin to obtain consent and release forms.

2) **DZ concordant twins:** We initiated efforts to obtain consent and release forms from 130 DZ concordant pairs, by sending letters first to twins who were diagnosed after 1975 and known be alive at last contact. We have also recently sent letters to the next of kin to those who were known to deceased. Currently we have obtained blocks from 39 or 15.0% of these 260 cases.

3) **MZ discordant twins:** We also selected 548 MZ discordant pairs who met the following criteria: a) they were diagnosed after 1975 and we had obtained their pathology report, and b) they had completed the epidemiologic questionnaire that was sent to all females pairs of twins with at least one member with breast cancer who participated in the International Twin Study Registry. We have received blocks from 124 (22.6%) of these cases.

Among concordant pairs for whom we have received blocks, we have 57 pairs with blocks received from both twins (50 MZ and 7 DZ) and 92 pairs with blocks received from one twin (67 MZ and 25 DZ). Thus, in total we have received blocks from at least one twin for 149 concordant pairs (117 MZ and 32 DZ). In addition we have received blocks from 124 of the 548 discordant MZ pairs. For some of these twins, the only blocks received were the ones without tumor tissue (we asked for both tumor and normal tissue). Thus of the 57 pairs with blocks from both, tumor tissue is available from both members of 45 of these pairs.

b. Immunohistochemistry for p53, HER-2/*neu*, ER, and PR
The percent of tumors that stained positive for each of the biomarkers is shown in Table 2. For all tumor tissues studied (including 6 cases with both right and left tumors) the percent positive ranged from a high of 67.5 for ER and a low of 10.4 for HER-2/neu, based on high expression of HER-2/neu. These results are consistent with other reports in the literature. Some differences by pair type are evident as ER, p53, and HER-2/neu were more likely to be positive higher among concordant pairs than discordant pairs.

Table 1: Status of twin participation and acquisition of blocks/slides by category of pair (as of 9/28/98)

Status	Total		MZ Con-cordant		DZ Con-cordant		MZ Dis-cordant	
			N	%	N	%	N	%
Total pairs	884		206		130		548	
Total individuals (cases)	1220	100.0	412	100.0	260	100.0	548	100.0
Resolved cases:								
Blocks/slides rec.	330	27.0	167	40.5	39	15.0	124	22.6
Blocks/slides n/a*	347	28.4	155	37.6	76	29.2	116	21.2
Twin refused	46	3.8	17	4.1	8	3.1	21	3.8
Total resolved	723	59.3	339	82.3	123	47.3	261	47.6
In process:								
Hosp. Pending	48	3.9	12	2.9	11	4.2	25	4.6
Consent Rec.	56	4.6	7	1.7	5	1.9	44	8.0
Patient Pending	393	32.2	54	13.1	121	46.6	218	39.8
Total in process	497	40.7	73	17.7	137	52.7	287	52.4

*largely consists of cases who were diagnosed before 1975

Table 2: Immunohistochemistry Results for Individual Cases by Pair type

		Pair type	
Percent Positive* for	Total	Concordant	Discordant
(N)	(261)	(180)	(81)
ER	67.5	71.1	59.3
PR	63.1	61.2	66.7
P53	26.1	29.1	19.8
HER-2/neu (M+H)	30.8	32.6	27.2
HER-2/neu (H)	10.4	11.8	7.4

*Positivity for ER, PR, and p53 defined as expression in more than 10% of cells; positivity for HER-2/neu defined as both medium or high expression (M+H) and high expression alone (H).

The correlation of positivity for different biomarkers within tumors by pair type is shown in Table 3A, 3B and 3C. As expected, ER and PR were highly correlated with each other in each subgroup (r=0.58, p<.05 among tumors from concordant pairs and r=0.53, p<.05 among tumors from discordant pairs). P53 was negatively correlated with ER, especially within tumors from concordant pairs. ER and PR were both negatively correlated with HER-2/neu when the definition of positivity for HER-2/neu was based solely on those expressing high levels. There was a slight non-significant positive correlation between p53 and HER-2/neu.

Table 3A: Correlation coefficients between tumor biomarkers within same tumor: All tumor tissues (N=260)

	ER	PR	p53	HER-2(M+H)	HER-2(H)
ER	1.00				
PR	0.55*	1.00			
p53	-0.16*	-0.06	1.00		
HER-2/neu (M+H)	-0.003	-0.02	0.10	1.00	
HER-2/neu(H)	-0.25*	-0.26*	0.06	0.51*	1.00

*p<.05

Table 3B: Correlation coefficients between tumor biomarkers within same tumor: All tumor tissues from concordant pairs (N=180)

	ER	PR	p53	HER-2(M+H)	HER-2(H)
ER	1.00				
PR	0.58*	1.00			
p53	-0.21*	-0.006	1.00		
HER-2/neu (M+H)	0.04	0.08	0.09	1.00	
HER-2/neu(H)	-0.35*	-0.24*	-0.001	0.53*	1.00

*p<.05

Table 3C: Correlation coefficients between tumor biomarkers within same tumor: All tumor tissues from discordant pairs (N=81)

	ER	PR	p53	HER-2(M+H)	HER-2(H)
ER	1.00				
PR	0.53*	1.00			
p53	-0.09	-0.18	1.00		
HER-2/neu (M+H)	-0.12	-0.27*	0.12	1.00	
HER-2/neu(H)	-0.05	-0.30*	0.21	0.46*	1.00

*p<.05

Concordancy of Biomarkers in Within Concordant Pairs

From the 180 twins from the concordant pairs with immunohistochemistry completed, there were 41 pairs (36 MZ and 5 DZ) included with results available from both members of the pair. We next looked to see if these markers were identical between members of the same pair with the supposition being that, if they were, it might indicate that predisposing genetic factors were largely in control of the development of these markers. Table 4 shows the correlation for each of these biomarkers between members from these concordant pairs. The highest level of correlation was for ER ($r=0.42$, $p<.05$). PR and p53 had similar levels of correlation ($r=.33$ and $.30$, respectively). No correlation between members of a pair was found for HER-2/neu. Kappa (Table 5), which takes into account chance agreement, was also the highest for ER (0.42, $p<.05$), and lowest for HER-2/neu (0.03).

Table 4: Correlation coefficients between tumor biomarkers of individuals from the same twin pair: All Concordant pairs (N=41 pairs) and MZ pairs (N=36)

Twin 2	Twin 1									
	ER		PR		p53		HER-2(M+H)		HER-2(H)	
	All	MZ	All	MZ	All	MZ	All	MZ	All	MZ
ER	0.42*	0.35*								
PR			0.33*	0.28						
p53					0.30	0.22				
HER-2/neu (M+H)							0.03	-0.03		
HER-2/neu(H)									0.004	0.006

*p<.05

Table 5: Measures of Agreement Between Biomarkers from Members of Concordant Pairs with Tissue Analyzed from Both Twins

41 pairs	Percent Agree	Percent Expected	Kappa
ER	73.7	54.8	0.42*
PR	63.4	47.8	0.30*
P53	70.7	58.5	0.30
HER-2/neu (M+H)	58.5	57.4	0.03
HER-2/neu (H)	73.2	73.0	0.004

*p<.05

c. DNA Sequencing of the p53 gene

The work of sequencing the entire p53 gene is well underway. The complete gene has been sequenced for 50 cases and mutations were detected in 25. We are re-requesting some tissue blocks to obtain additional tissue for this work. Work in this area will be completed during the next year.

d. FISH
We have completed FISH analyses to quantify HER-2/*neu* gene amplification for approximately 100 cases at this time. This work is ongoing.

e. Epidemiological Analyses: Association with Risk Factors
We will complete these analyses in our final report. Preliminary analyses were presented in last year's report.

C. CONCLUSIONS
We have been granted a 1 year no cost extension to complete the work on this project. We will continue to obtain tissue blocks through Dec. 31, 1998. The additional year extension will include the completion of immunohistochemistry on all blocks received by Dec. 31, 1998, the completion p53 sequencing on all breast cancer concordant pairs with tumor blocks obtained from both twins (regardless of p53 immunohistochemistry results), and FISH to detect amplification of the HER-2/neu gene on the above mentioned concordant pairs. Analyses of the data will address concordance of these tumor markers within the same tumor tissue and within twin pairs, and look at associations of these markers with environmental exposures. In addition, among the breast cancer discordant pairs, we will conduct stratified analyses based on tumor characteristics to determine if specific risk factors are associated with the development of breast cancer that is positive or negative for the tumor characteristics under study, i.e. p53, HER-2/neu, and ER and PR receptors.

D. REFERENCES

1) Lane, D. and Benchimol, S. 1990. p53: oncogene or antioncogene? Genes Develop. 4:1.
2) Wang, N., To, H., Lee, W., and Lee, E. 1993. Tumor suppressor activity of RB and p53 genes in human breast carcinoma cells. Oncogene 8:279-288.
3) Prosser, J., Elder, P., Condie, A., MacFadyen, I., Steel, C., and Evans, H. 1991. Mutations in p53 do not account for heritable breast cancer: a study in five affected families. Br. J. Cancer 63:181-4.
4) Nigro, J. et. al. 1989. Nature 342:705.
5) Soussi, T. et al. 1990. Oncogene 5:945.
6) Prosser, J., Porter, D., Coles, C., Condie, A., Thompson, A., Chetty, U., Steel, C., and Evans, H. 1992. Constitutional p53 mutation in a non-Li-Fraumeni family. Br. J. Cancer 65:527-528.
7) Harris, C., Hollstein, M. 1993. Clinical Implications of the p53 tumor-suppressor gene. NEJM 329:1318-1327.
8) Davidoff, A., Kerns, B., Pence, J., Marks, J., Iglehart, D. 1991. p53 alterations in all stages of breast cancer. Journal of Surgical Oncology 48:260-267.
9) Thompson, A., Anderson, T., Condie, A., Prosser, J., Chetty, U., Carter, D., Evans, H., Steel, C. 1992. p53 allele losses, mutations, and expression in breast cancer and their relationship to clinico-pathological parameters. Int. J. Cancer 50:528-532.
10) Singh, S., Simon, M., Meybohm, I., Jantke, I., Jonat, W., Maass, H., and Goedde. 1993. Human breast cancer: frequent p53 allele loss and protein overexpression. Hum Genet. 90:635-

640.

11) Chen, L., Neubauer, A., Kurisu, W., Waldman, F., Ljung, B., Goodson, W., Goldman, E., Moore, D., Balazs, M., Liu, E., Mayall, B., Smith, H. 1991. Loss of heterozygosity on the short arm of chromosome 17 is associated with high proliferative capacity and DNA aneuploidy in primary human breast cancer. Proc. Natl. Acad. Sci. USA 88:3847-3851.

12) Finlay, C., Hinds, P., Levine, A. 1989. The p53 proto-oncogene can act as a suppressor of transformation. Cell 57:1083-1093.

13) Barnes, D., Hanby, A., Gillett, C., Mohammed, S., Hodgson, S., Bobrow, L., Leigh, I., Purkis, T., MacGeoch, C., Spurr, N., Bartek, J., Vojtesek, B., Picksley, S., Lane, D. 1992. Abnormal expression of wild type p53 protein in normal cells of a cancer family patient. Lancet 340:259-63.

14) Hollstein M, Sidransky, Vogelstein B, Harris C. 1991. P53 mutations in human cancers. Science 253: 49-53.

15) Moll, U., Riou, G., and Levine, A. (1992). Two distinct mechanisms alter p53 in breast cancer: mutation and nuclear exclusion. Proc. Natl. Acad. Sci. USA 89:7262-7266.

16) Domagala, W., Harezga, B., Szadowska, A., Markiewski, M., Weber, K., and Osborn, M. (1993). Nuclear p53 protein accumulates preferentially in medullary and high-grade ductal but rarely in lobular breast carcinomas. Am J. Path. 142:669-674.

17) Malkin, D., Li, F., Strong, L., Fraumeni, J. Jr., Nelson, C., Kim, D., Kassel, J., Gryka, M., Bischoff, F., Tainsky, M., and Friend, S. 1990. Germ line p53 mutations in familial syndrome of breast cancer, sarcomas, and other neoplasms. Science 250:1233-1238.

18) Prosser, J., Elder, P., Condie, A., MacFadyen, I., Steel, C., Evans, H. 1991. Mutations in p53 do not account for heritable breast cancer: a study in five affected families. Br. J. Ca. 63:181-4.

19) Warren, W., Eeles, R., Ponder, B., Easton, D., Averill, D., Ponder, M., Anderson, K., Evans, A., DeMars, R., Love, R., Dundas, S., Stratton, M., Trowbridge, P., Cooper, C., and Peto, J. 1992. No evidence for germline mutations in exons 5-9 of the p53 gene in 25 breast cancer families. Oncogene 7:1043-1046.

20) Lidereau, R., and Soussi, T. 1992. Absence of p53 germ-line mutations in bilateral breast cancer patients. Hum. Genet. 89:250-252.

21) Coles, C., Thompson, A., Elder, P., Cohen, B., Mackenzie, I., Cranston, G., Chetty, U., Mackay, J., Macdonald, M., Nakamura, Y., Hoyheim, B., and Steel, C. 1990. Evidence implicating at least two genes on chromosome 17p in breast carcinogenesis. Lancet 336:761-763.

22) van de Vijver, M. 1993. Molecular genetic changes in human breast cancer. Advances in Cancer Research 61:25-56.

23) Poller DN, Hutchings CE, Galea M, Bell JA, Nicholson RA, Elston CW, Blamey RW, Ellis IO. p53 protein expression in human breast carcinoma: relationship to expression of epidermal growth factor receptor, c-erbB-2 protein overexpression and estrogen receptor. Br J Cancer 1992; 66:583-588.

24) Lipponen, H., Aaltomaa, S., Syrjanen, S., Syrjanen, K. 1993. c-erbB-2 oncogene related to p53 expression, cell proliferation, and prognosis in breast cancer. Anticancer Research 13:1147-1152.

25) Knyazev, P., Imyanitov, E., Chernitsa, O., Nikiforova, I. 1993. Loss of heterozygosity at chromosome 17p is associated with HER-2 amplification and lack of nodal invovement in breast cancer. Int. J. Cancer 53:11-16.

26) Barbareschi, M., Leonardi, E., Mauri, F., Serio, G. and Dalla Palma P. (1992). p53 and C-erbB-2 protein expression in Breast Carcinomas. Am J Clin Pathol 98:408-418.

27) Horak, E., Smith, K, Bromley, L., LeJeune, S., Greenall, M., Lane, D., and Harris, A. (1991). Mutant p53, EGF receptor and C-erbB-2 expression in human breast cancer. Oncogene 6:2277-2284.

28) Walker, R., Dearing, S., Lane, D., and Varley, J. (1991). Expression of p53 protein in infiltrating and in-situ breast carcinomas. Journal of Pathology 165:203-211.

29) Press, M., Pike, M., Chazin, V., Hung, G., Udove, J., Markowicz, M., Danyluk, J., Godolphin, W., Sliwkowski, M., Akita, R., Paterson, M., Slamon, D. 1993. Her-2/neu in node-negative breast cancer: direct tissue quantitation by computerized image analysis and association of overexpression with increased risk of recurrent disease. Cancer Research 53:4960-4970.

30) Thor, A., Moore, D., Edgerton, S., Kawasaki, E., Reihsaus, E., Lynch, H. Marcus, J., Schwartz, L., Chen, L., Mayall, B. and Smith, H. 1992. Accumulation of p53 tumor suppressor gene protein: an independent marker of prognosis in breast cancers. J Natl Cancer Inst 84:845-855.

31) McTiernan, A., Thomas, D., Johnson, L., Roseman, D. 1986. Risk factors for estrogen-rich and estrogen-poor breast cancers. JNCI 77:849-854.

32) Treurniet, H., Rookus, M., Peterse, H., Hart, A., and van Leeuwen, F. (1992). Differences in breast cancer risk factors to neu (c-erbB-2) protein overxpression of the breast tumor. Cancer Research 52:2344-2345.

33) Harris, A. 1992. p53 expression in human breast cancer. Advances in Cancer Research 59:69-88.

34) Deapen, D., Horwitz, D., Escalante, A., Weinrib, L., Roy-Burman, P., Walker, A., Mack, T. 1992. A revised estimate of twin concordance in SLE. Arth and Rheum 35:

35) Van de Vijver MJ, Peterse JL, Mooi WJ, Wisman P, Lomans J, Dalesio O, Nusse R. 1988. Neu-protein overexpression in breast cancer. Association with comedo-type ductal carcinoma in situ and limited prognostic value in stage II breast cancer. N. Engl. J. Med. 319: 1239-1245.

36) Press, M., Hung, G., Godolphin, W., Slamon, D. 1993. Sensitivity of HER-2/neu antibodies in archival tissue samples: potential source of error in immunohistochemical studies of expression. Cancer Research (In press).

37) Press, M., Hung, G., Pike, M., George, J., Dietz-Band, J., James, W., Slamon, D., Batsakis, J., El-Naggar, A. 1993. Amplification and overexpression of HER-2/neu in carcinomas of the salivary gland: correlation with poor prognosis. (In review).

38) Slamon, DJ, Press MF, Godolphin W, Jones LA, Holt JA, Stuart SG, Ullrich A. 1989a. The HER-2/neu proto-oncogene in human breast cancer. Cancer Cells 7: 371-380.

39) Slamon, D., Godolphin, W., Jones, L., Holt, J., Wong, S., Keith, D., Levin, w., Stuart, s., Udove, J., Ullrich, A., et al. 1989b. Studies of the HER-2/neu proto-oncogene in human breast and ovarian cancer. Science 244:707-12.

40) Press MF, Cordon-Cardo C, Slamon DJ. 1990. Expression of the HER-2/neu Proto-oncogene in Normal Adult and Fetal Tissues. Oncogene 5: 953-962.

41) Coussens L, Yang-Feng TL, Chen Y-C L E, Gray A, McGrath J, Seeburg PH, Libermann TA, Schlessinger J, Francke U, Levinson A, Ullrich A. 1985. Tyrosine kinase receptor with extensive homology to EGF receptor shares chromosomal location with neu oncogene. Science 230: 1132-1139.

42) Slamon DJ, Clark GM, Wong SG, Levin WJ, Ullrich A, McGuire WL. 1987. Human breast cancer: Correlation of relapse and survival with amplification of the HER-2/neu oncogene. Science 235: 177-182.

43) Shibata D, Hu E, Weiss LM, Brynes RK, Nathwani BN. 1990. Detection of specific t(14;18) chromosomal translocations in fixed tissues. Human Pathology 21: 199-203.

44) Jackson DP, Lewis FA, Taylor GR, Boylston AW, Quirke P. 1990. Tissue extraction of DNA and RNA and analysis by the polymerase chain reaction. J. Clin. Pathol. 43: 499-504. 45) Rogers BB, Alpert LC, Hine EAS, Buffone J. 1990. Analysis of DNA in fresh and fixed tissue by the polymerase chain reaction. Am. J. Pathol. 136: 541-548.

46) Saiki RK, Gelfand DH, Stoffel S, Scharf SJ, Higuchi R, Horn GT, Mullis KB, Erlich HA. 1990. Primer-directed enzymatic amplification of DNA with a thermostable DNA polymerase. Science 239: 487-491.

47) Sarkar G, Sommer SS. 1990. Shedding light on PCR contamination. Nature 343: 27.

48) Hensel CH, Xiang RH, Sakaguchi AY, Naylor SL. 1991. Use of the single strand conformation polymorphism technique and PCR to detect p53 gene mutations in small cell lung cancer. Oncogene 6: 1067-1071.

49) Sanger F, Nicklen S, Coulson AR. 1977. Proc. Natl. Acad. Sci. USA 74: 5463-5467. 50) Fleiss, Joseph L. 1981. Statistical Methods for Rates and Proportions, Second Edition. John Wiley and Sons:NY.

51) Buckley J. Epilog, 1990, Pasadena